Applicant: Soto, et al.
USSN: 09/512,581

APPENDIX A

TABLE 1. CLUSTALW alignment of SEQ ID NO: 2 ("SID2") and murine AS3 polypeptide (mAS3) as disclosed in GenBank Accession No. AY102267.

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SID2:    1    MAHSKTRTNDGKITYPPGVKEISDKISKEEMVRRLKMVVKTFMDMDQDSEEEKELYLNLA  60
              MAHSKTRTNDGKITYPPGVKEISDKISKEEMVRRLKMVVKTFMDMDQDSEEEKELYLNLA
MAS3:    1    MAHSKTRTNDGKITYPPGVKEISDKISKEEMVRRLKMVVKTFMDMDQDSEEEKELYLNLA  60

SID2:   61    LHLASDFFLKHPGKDVRLLVACCLADIFRIYAPEAPYTSPDKLKDIFMFITRQLKGLEDT  120
              LHLASDFFLKHP KDVRLLVACCLADIFRIYAPEAPYTSPDKLKDIFMFITRQLKGLEDT
MAS3:   61    LHLASDFFLKHPDKDVRLLVACCLADIFRIYAPEAPYTSPDKLKDIFMFITRQLKGLEDT  120

SID2:  121    KSPQFNRYFYLLENIAWVKSYNICFELEDSNEIFTQLYRTLFSVINNGHNQKVHMHMVDL  180
              KSPQFNRYFYLLENIAWVKSYNICFELEDSNEIFTQLYRTLFSVINNGHNQKVHMHMVDL
MAS3:  121    KSPQFNRYFYLLENIAWVKSYNICFELEDSNEIFTQLYRTLFSVINNGHNQKVHMHMVDL  180

SID2:  181    MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITTFFNQV  240
              MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYIT FFNQV
MAS3:  181    MSSIICEGDTVSQELLDTVLVNLVPAHKNLNKQAYDLAKALLKRTAQAIEPYITNFFNQV  240

SID2:  241    LMLGKTSISDLSEHVFDLILELYNIDSHLLLSVLPQLEFKLKSNDNEERLQVVKLLAKMF  300
              LMLGKTSISDLSEHVFDLILELYNIDSHLLLSVLPQLEFKLKSNDNEERLQVVKLLAKMF
MAS3:  241    LMLGKTSISDLSEHVFDLILELYNIDSHLLLSVLPQLEFKLKSNDNEERLQVVKLLAKMF  300

SID2:  301    GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH  360
              GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH
MAS3:  301    GAKDSELASQNKPLWQCYLGRFNDIHVPIRLECVKFASHCLMNHPDLAKDLTEYLKVRSH  360

SID2:  361    DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYA  420
              DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKY+
MAS3:  361    DPEEAIRHDVIVSIVTAAKKDILLVNDHLLNFVRERTLDKRWRVRKEAMMGLAQIYKKYS  420

SID2:  421    LQSAAGKDAAKQIAWIKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL  480
              LQSAAGKDAAKQI+W+KDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL
MAS3:  421    LQSAAGKDAAKQISWVKDKLLHIYYQNSIDDRLLVERIFAQYMVPHNLETTERMKCLYYL  480

SID2:  481    YATLDLNAVKALNEMWKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG  540
              YATLDLNAVKALNEM KCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG
MAS3:  481    YATLDLNAVKALNEMRKCQNLLRHQVKDLLDLIKQPKTDASVKAIFSKVMVITRNLPDPG  540

SID2:  541    KAQDFMKKFTQVLEDDEKIRKQLEVLVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM  600
              KAQDFMKKFTQVLEDDEKIRKQLE LVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM
MAS3:  541    KAQDFMKKFTQVLEDDEKIRKQLEALVSPTCSCKQAEGCVREITKKLGNPKQPTNPFLEM  600

SID2:  601    IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH  660
              IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH
MAS3:  601    IKFLLERIAPVHIDTESISALIKQVNKSIDGTADDEDEGVPTDQAIRAGLELLKVLSFTH  660

SID2:  661    PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK  720
              PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK
MAS3:  661    PISFHSAETFESLLACLKMDDEKVAEAALQIFKNTGSKIEEDFPHIRSALLPVLHHKSKK  720

SID2:  721    GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ  780
              GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ
MAS3:  721    GPPRQAKYAIHCIHAIFSSKETQFAQIFEPLHKSLDPSNLEHLITPLVTIGHIALLAPDQ  780

SID2:  781    FAAPWKSWVATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK  840
              FAAP KS VATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK
MAS3:  781    FAAPLKSLVATFIVKDLLMNDRLPGKKTTKLWVPDEEVSPETMVKIQAIKMMVRWLLGMK  840
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SID2:   841  NNHSKSGTSTLRLLTTILHSDGDLTEQGKISKPDMSRLRLAAGSAIVKLAQEPCYHEIIT  900
             NNHSKSGTSTLRLLTTILHSDGDLTEQGKISKPDMSRLRLAAGSAIVKLAQEPCYHEIIT
MAS3:   841  NNHSKSGTSTLRLLTTILHSDGDLTEQGKISKPDMSRLRLAAGSAIVKLAQEPCYHEIIT  900

SID2:   901  LEQYQLCALAINDECYQVRQVFAQKLHKGLSRLRLPLEYMAICALCAKDPVKERRAHARQ  960
             LEQYQLCALAINDECYQVRQVFAQKLHKGLSRLRLPLEYMAICALCAKDPVKERRAHARQ
MAS3:   901  LEQYQLCALAINDECYQVRQVFAQKLHKGLSRLRLPLEYMAICALCAKDPVKERRAHARQ  960

SID2:   961  CLVKNINVRREYLKQHAAVSEKLLSLLPEYVVPYTIHLLAHDPDYVKVQDIEQLKDVKEC  1020
             CLVKN  VRREYLKQHA+VSEKLLSLLPEYVVPYTIHLLAHDPDYVKVQDIEQLKDVKEC
MAS3:   961  CLVKNTTVRREYLKQHASVSEKLLSLLPEYVVPYTIHLLAHDPDYVKVQDIEQLKDVKEC  1020

SID2:  1021  LWFVLEILMAKNENNSHAFIRKMVENIKQTKDAQGPDDAKMNEKLYTVCDVAMNIIMSKS  1080
             LWFVLEILMAKNENNSHAFIRKMVENIKQTKDAQGPDD KMNEKLYTVCDVAMNIIMSKS
MAS3:  1021  LWFVLEILMAKNENNSHAFIRKMVENIKQTKDAQGPDDTKMNEKLYTVCDVAMNIIMSKS  1080

SID2:  1081  TTYSLESPKDPVLPARFFTQPDKNFSNTKNYLPPEMKSFFTPGKPKTTNVLGAVNKPLSS  1140
             TTYSLESPKDPVLPARFFTQPDKNFSNTKNYLPPEMKSFFTPGKPKT NVLGAVNKPLSS
MAS3:  1081  TTYSLESPKDPVLPARFFTQPDKNFSNTKNYLPPEMKSFFTPGKPKTANVLGAVNKPLSS  1140

SID2:  1141  AGKQSQTKSSRMETVSNASSSSNPSSPGRIKGRLDSSEMDHSENEDYTMSSPLPGKKSDK  1200
             AGKQSQTKSSRMETVSNASSSSNPSSPGRIKGRLDSSEMDHSENEDYTMSSPLPGKKSDK
MAS3:  1141  AGKQSQTKSSRMETVSNASSSSNPSSPGRIKGRLDSSEMDHSENEDYTMSSPLPGKKSDK  1200

SID2:  1201  RDDSDLVRSELEKPRGRKKTPVTEQEEKLGMDDLTKLVQEQKPKGSQRSRKRGHTASESD  1260
              R+D DL  SELEKPR RKK PVT+ EEKLGMDDLTKLVQEQKPKGSQR RKRG TAS+SD
MAS3:  1201  REDPDL--SELEKPRSRKKAPVTDPEEKLGMDDLTKLVQEQKPKGSQRGRKRGRTASDSD  1258

SID2:  1261  EQQWPEEKRLKEDILENEDEQNSPPKKGKRGRPPKPLGGGTPKEEPTMKTSKKGSKKKSG  1320
             EQQWPEEKR KE++LENEDEQNSPPKKGKRGRPPKPLGGGT KEEPTMKTSKKG+KKK
MAS3:  1259  EQQWPEEKRHKEELLENEDEQNSPPKKGKRGRPPKPLGGGTSKEEPTMKTSKKGNKKKLV  1318

SID2:  1321  PPAPEEEEEEERQSGNTEQKSKSKQHRVSRRAQQRAESPESSAIESTQSTPQKGRGRPSK  1380
             PP  +++EEEERQ GNTE KSKSKQHR S+RAQQRAESPE+SA+ESTQSTPQKGRGRPSK
MAS3:  1319  PPVVDDDEEEERQIGNTEHKSKSKQHRTSKRAQQRAESPETSAVESTQSTPQKGRGRPSK  1378

SID2:  1381  TPSPSQPKKNV  1391
              PSPSQP K +
MAS3:  1379  APSPSQPPKKI  1389
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